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SEQUENCE LISTING

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<120> PROTEIN TRANSDUCING DOMAIN/DEAMINASE
CHIMERIC PROTEINS, RELATED COMPOUNDS, AND USES THEREOF

<130> 21108.0034U2

<140> 10/523,038
<141>

<150> PCT/US03/24458
<151> 2003-08-05

<150> 60/419,982
<151> 2002-10-21

<150> 60/401,293
<151> 2002-08-05

<160> 49

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 384
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 1
Met Lys Pro His Phe Arg Asn Thr Val Glu Arg Met Tyr Arg Asp Thr
1 5 10 15
Phe Ser Tyr Asn Phe Tyr Asn Arg Pro Ile Leu Ser Arg Arg Asn Thr
20 25 30
Val Trp Leu Cys Tyr Glu Val Lys Thr Lys Gly Pro Ser Arg Pro Pro
35 40 45
Leu Asp Ala Lys Ile Phe Arg Gly Gln Val Tyr Ser Glu Leu Lys Tyr
50 55 60
His Pro Glu Met Arg Phe Phe His Trp Phe Ser Lys Trp Arg Lys Leu
65 70 75 80
His Arg Asp Gln Glu Tyr Glu Val Thr Trp Tyr Ile Ser Trp Ser Pro
85 90 95
Cys Thr Lys Cys Thr Arg Asp Met Ala Thr Phe Leu Ala Glu Asp Pro
100 105 110
Lys Val Thr Leu Thr Ile Phe Val Ala Arg Leu Tyr Tyr Phe Trp Asp
115 120 125

Pro Asp Tyr Gln Glu Ala Leu Arg Ser Leu Cys Gln Lys Arg Asp Gly
130 135 140
Pro Arg Ala Thr Met Lys Ile Met Asn Tyr Asp Glu Phe Gln His Cys
145 150 155 160
Trp Ser Lys Phe Val Tyr Ser Gln Arg Glu Leu Phe Glu Pro Trp Asn
165 170 175
Asn Leu Pro Lys Tyr Tyr Ile Leu Leu His Ile Met Leu Gly Glu Ile
180 185 190
Leu Arg His Ser Met Asp Pro Pro Thr Phe Thr Phe Asn Phe Asn Asn
195 200 205
Glu Pro Trp Val Arg Gly Arg His Glu Thr Tyr Leu Cys Tyr Glu Val
210 215 220
Glu Arg Met His Asn Asp Thr Trp Val Leu Leu Asn Gln Arg Arg Gly
225 230 235 240
Phe Leu Cys Asn Gln Ala Pro His Lys His Gly Phe Leu Glu Gly Arg
245 250 255
His Ala Glu Leu Cys Phe Leu Asp Val Ile Pro Phe Trp Lys Leu Asp
260 265 270
Leu Asp Gln Asp Tyr Arg Val Thr Cys Phe Thr Ser Trp Ser Pro Cys
275 280 285
Phe Ser Cys Ala Gln Glu Met Ala Lys Phe Ile Ser Lys Asn Lys His
290 295 300
Val Ser Leu Cys Ile Phe Thr Ala Arg Ile Tyr Asp Asp Gln Gly Arg
305 310 315 320
Cys Gln Glu Gly Leu Arg Thr Leu Ala Glu Ala Gly Ala Lys Ile Ser
325 330 335
Ile Met Thr Tyr Ser Glu Phe Lys His Cys Trp Asp Thr Phe Val Asp
340 345 350
His Gln Gly Cys Pro Phe Gln Pro Trp Asp Gly Leu Asp Glu His Ser
355 360 365
Gln Asp Leu Ser Gly Arg Leu Arg Ala Ile Leu Gln Asn Gln Glu Asn
370 375 380

<210> 2

<211> 1155

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 2

atgaagcctc	acttcagaaa	cacagtggag	cgaatgtatc	gagacacatt	ctcctacaac	60
ttttataata	gacccatcct	ttctcgtcg	aataccgtct	ggctgtgcta	cgaagtga	120
acaaagggtc	cctcaaggcc	ccctttggac	gcaaagatct	ttcgaggcca	ggtgtattcc	180
gaacttaagt	accaccaga	gatgagattc	ttccactgg	tcagcaagt	gaggaagctg	240
catcgtgacc	aggagtatga	ggtcacctgg	tacatatcct	ggagccccctg	cacaaagtgt	300
acaagggata	tggccacggt	cctggccgag	gacccgaagg	ttaccctgac	catcttcggt	360
gcccgcctct	actacttctg	ggacccagat	taccaggagg	cgcttcgcag	cctgtgtcag	420
aaaagagacg	gtccgcgtgc	caccatgaag	atcatgaatt	atgacgaatt	tcagcactgt	480
tggagcaagt	tcgtgtacag	ccaaagagag	ctatttgagc	cttggaataa	tctgcctaaa	540
tattatatat	tactgcacat	catgctgggg	gagattctca	gacactcgat	ggatccaccc	600
acattcactt	tcaactttaa	caatgaacct	tgggtcagag	gacggcatga	gacttacctg	660
tgttatgagg	tggagcgcac	gcacaatgac	acctgggtcc	tgctgaacca	gcgcaggggc	720
tttctatgca	accaggctcc	acataaacac	ggtttccttg	aaggccgcca	tgcatagctg	780

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tgcttcctgg acgtgattcc cttttggaag ctggacctgg accaggacta cagggttacc      840
tgcttcacct cctggagccc ctgcttcagc tgtgcccagg aaatggctaa attcatttca      900
aaaaacaaac acgtgagcct gtgcatcttc actgcccgcg tctatgatga tcaaggaaga      960
tgtcaggagg ggctgcgcac cctggccgag gctggggcca aaatttcaat aatgacatac     1020
agtgaattta agcactgctg ggacaccttt gtggaccacc agggatgtcc cttccagccc     1080
tgggatggac tagatgagca cagccaagac ctgagtggga ggctgcgggc cattctccag     1140
aatcaggaaa actga                                     1155

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<210> 3

<211> 198

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 3

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Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
 1           5           10           15
Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
      20           25           30
Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
      35           40           45
Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
      50           55           60
Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
      65           70           75           80
Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
      85           90           95
Phe Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg
      100          105          110
Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
      115          120          125
Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr
      130          135          140
Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys
      145          150          155          160
Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu
      165          170          175
Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala
      180          185          190
Phe Arg Thr Leu Gly Leu
      195

```

<210> 4

<211> 597

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 4

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atggacagcc tcttgatgaa ccggaggaag tttctttacc aattcaaaaa tgtccgctgg      60

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gctaagggtc ggcgtgagac ctacctgtgc tacgtagtga agaggcgtga cagtgtctaca 120
tcctttttcac tggacttttg ttatctttgc aataagaacg gctgccacgt ggaattgctc 180
ttcctccgct acatctcgga ctgggacctg gacctgggcc gctgctaccg cgtcacctgg 240
ttcacctcct ggagccccctg ctacgactgt gcccgcacatg tggccgactt tctgcgaggg 300
aaccccaacc tcagtctgag gatcttcacc gcgcgcctct acttctgtga ggaccgcaag 360
gctgagccccg aggggctgcg gcggctgcac cgcgccgggg tgcaaatagc catcatgacc 420
ttcaaagatt atttttactg ctggaatact tttgtagaaa accatgaaag aactttcaaa 480
gcctgggaag ggctgcatga aaattcagtt cgtctctcca gacagcttcg gcgcacacct 540
ttgccccctgt atgaggttga tgacttacga gacgcatttc gtactttggg actttga 597

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<210> 5

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 5

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Met Thr Ser Glu Lys Gly Pro Ser Thr Gly Asp Pro Thr Leu Arg Arg
 1           5           10           15
Arg Ile Glu Pro Trp Glu Phe Asp Val Phe Tyr Asp Pro Arg Glu Leu
          20           25           30
Arg Lys Glu Ala Cys Leu Leu Tyr Glu Ile Lys Trp Gly Met Ser Arg
        35           40           45
Lys Ile Trp Arg Ser Ser Gly Lys Asn Thr Thr Asn His Val Glu Val
       50           55           60
Asn Phe Ile Lys Lys Phe Thr Ser Glu Arg Asp Phe His Pro Ser Ile
 65           70           75           80
Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Trp Glu Cys
          85           90           95
Ser Gln Ala Ile Arg Glu Phe Leu Ser Arg His Pro Gly Val Thr Leu
        100          105          110
Val Ile Tyr Val Ala Arg Leu Phe Trp His Met Asp Gln Gln Asn Arg
       115          120          125
Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln Ile Met
      130          135          140
Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe Val Asn Tyr Pro
 145          150          155          160
Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro Pro Leu Trp Met Met
          165          170          175
Leu Tyr Ala Leu Glu Leu His Cys Ile Ile Leu Ser Leu Pro Pro Cys
        180          185          190
Leu Lys Ile Ser Arg Arg Trp Gln Asn His Leu Thr Phe Phe Arg Leu
       195          200          205
His Leu Gln Asn Cys His Tyr Gln Thr Ile Pro Pro His Ile Leu Leu
      210          215          220
Ala Thr Gly Leu Ile His Pro Ser Val Ala Trp Arg
 225          230          235

```

<210> 6

<211> 863

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 6

gatcccagag	gaggaagtcc	agagacagag	caccatgact	tctgagaaag	gagaagaatc	60
gaaccctggg	agtttgacgt	cttctatgac	cccagagaac	ttcgtaaaga	ggcctgtctg	120
ctctacgaaa	tcaagtgggg	catgagccgg	aagatctggc	gaagctcagg	caaaaacacc	180
accaatcacg	tggaagttaa	ttttataaaa	aaatttacgt	cagaaagaga	ttttcaccca	240
tccatcagct	gtccatcac	ctggttcttg	tcctggagtc	cctgctggga	atgctcccag	300
gctattagag	agtttctgag	tcggcaccct	ggtgtgactc	tagtgatcta	cgtagctcgg	360
cttttttggc	acatggatca	acaaaatcgg	caaggctctca	gggaccttgt	taacagtgga	420
gtaactattc	agattatgag	agcatcagag	tattatcact	gctggaggaa	ttttgtcaac	480
taccacactg	gggatgaagc	tcactggcca	caataccac	ctctgtggat	gatgttgtag	540
gcactggagc	tgcactgcat	aattctaagt	cttccaccct	gtttaaagat	ttcaagaaga	600
tggcaaaatc	atcttacatt	tttcagactt	catcttcaaa	actgccatta	ccaaacgatt	660
ccgccacaca	tccttttagc	tacagggctg	atacatcctt	ctgtggcttg	gagatgaata	720
ggatgattcc	gtgtgtgtac	tgattcaaga	acaagcaatg	atgaccact	aaagagtga	780
tgccatttag	aatctagaaa	tgttcacaag	gtaccccaaa	actctgtagc	ttaaaccaac	840
aataaatatg	tattacctct	ggc				863

<210> 7

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 7

Met	Glu	Asn	Arg	Trp	Gln	Val	Met	Ile	Val	Trp	Gln	Val	Asp	Arg	Met
1				5					10					15	
Arg	Ile	Lys	Thr	Trp	Lys	Ser	Leu	Val	Lys	His	His	Met	Tyr	Ile	Ser
			20					25					30		
Lys	Lys	Ala	Lys	Glu	Trp	Val	Tyr	Arg	His	His	Tyr	Glu	Ser	Thr	His
		35					40					45			
Pro	Arg	Ile	Ser	Ser	Glu	Val	His	Ile	Pro	Leu	Gly	Asp	Ala	Lys	Leu
		50				55					60				
Val	Ile	Thr	Thr	Tyr	Trp	Gly	Leu	His	Thr	Gly	Glu	Arg	Glu	Trp	His
65					70				75					80	
Leu	Gly	Gln	Gly	Val	Ser	Ile	Glu	Trp	Arg	Lys	Lys	Arg	Tyr	Asn	Thr
			85					90						95	
Gln	Val	Asp	Pro	Asp	Leu	Ala	Asp	Lys	Leu	Ile	His	Leu	His	Tyr	Phe
			100					105					110		
Asp	Cys	Phe	Ser	Asp	Ser	Ala	Ile	Arg	His	Ala	Ile	Leu	Gly	His	Arg
		115				120						125			
Val	Arg	Pro	Lys	Cys	Glu	Tyr	Gln	Ala	Gly	His	Asn	Lys	Val	Gly	Ser
		130				135					140				
Leu	Gln	Tyr	Leu	Ala	Leu	Thr	Ala	Leu	Ile	Thr	Pro	Lys	Lys	Ile	Lys
145				150					155					160	
Pro	Pro	Leu	Pro	Ser	Val	Arg	Lys	Leu	Thr	Glu	Asp	Arg	Trp	Asn	Lys
			165					170						175	
Pro	Gln	Lys	Thr	Lys	Gly	His	Arg	Gly	Ser	His	Thr	Met	Asn	Gly	His
		180						185					190		

<210> 8
 <211> 569
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 8	
gatggcaggt gatgattgtg tggcaagtag acaggatgag gattaaaaca tggaaaagtt	60
tagtaaaaca ccatatgtat atttcaaaga aagctaagga atgggtctat agacatcact	120
atgaaagcac tcatccaaga ataagttcag aagtacacat ccactaggg gatgctaaat	180
tagtaataac aacatatttg ggtctgcata caggagaaaag agaatggcat ctgggtcagg	240
gagtcctccat agaatggagg aaaaagagat ataatacaca agtagaccct gacctagcag	300
acaaactaat ccacctgcat tattttgatt gtttttcaga ctctgctata agacatgccca	360
tattaggaca tagagttagg cctaagtgtg aatatcaagc aggacataac aaggtagggt	420
ctctacagta cttggcacta acagcattaa taacacccaaa aaagataaag ccacctttgc	480
ctagtgttag gaaactaaca gaggatagat ggaacaagcc ccagaagacc aagggccaca	540
gaggagacca tacaatgaat ggacactag	569

<210> 9
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 9
 Arg Gly Tyr Trp
 1

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 10	
cactttaggg agggctgtcc	20

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 11
ctgtgatcag ctggagatgg 20

<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 12
ctcccatggc aaagcctcac ttcagaaaca cag 33

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 13
ctcctcgagg ttttctgat tctggagaat ggccc 35

<210> 14
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 14
Gln Gln Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr
1 5 10 15
Ile Gln Ile Met Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe
20 25 30
Val Asn Tyr Pro Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro Pro
35 40 45
Leu Trp Met
50

<210> 15
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 15
 Pro Glu Thr Gln Gln Asn Leu Cys Arg Leu Val Gln Glu Gly Ala Gln
 1 5 10 15
 Val Ala Ala Met Asp Leu Tyr Glu Phe Lys Lys Cys Trp Lys Lys Phe
 20 25 30
 Val Asp Asn Gly Gly Arg Arg Phe Arg Pro Trp Lys Arg Leu Leu Thr
 35 40 45
 Asn Phe Arg
 50

<210> 16
 <211> 48
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 16
 Asp Gln Gln Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val
 1 5 10 15
 Thr Ile Gln Ile Met Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn
 20 25 30
 Phe Val Asn Tyr Pro Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro
 35 40 45

<210> 17
 <211> 47
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 17
 Lys Arg Pro Phe Gln Lys Gly Leu Cys Ser Leu Trp Gln Ser Gly Ile
 1 5 10 15
 Leu Val Asp Val Met Asp Leu Pro Gln Phe Thr Asp Cys Trp Thr Asn
 20 25 30
 Phe Val Asn Pro Lys Arg Pro Phe Trp Pro Trp Lys Gly Leu Glu
 35 40 45

<210> 18
 <211> 51
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 18

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Gln Gln Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr
 1           5           10           15
Ile Gln Ile Met Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe
          20           25           30
Val Asn Tyr Pro Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro Pro
      35           40           45
Leu Trp Met
    50

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<210> 19

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 19

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Pro Glu Asn Gln Gln Asn Leu Cys Arg Leu Val Gln Glu Gly Ala Gln
 1           5           10           15
Val Ala Ala Met Asp Leu Tyr Glu Phe Lys Lys Cys Trp Lys Lys Phe
          20           25           30
Val Asp Asn Gly Gly Arg Arg Phe Arg Pro Trp Lys Lys Leu Leu Thr
      35           40           45
Asn Phe Arg
    50

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<210> 20

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 20

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Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln
 1           5           10           15
Ile Met Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe Val Asn
          20           25           30
Tyr Pro Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro
      35           40           45

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<210> 21

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 21
Phe Gln Lys Gly Leu Cys Ser Leu Trp Gln Ser Gly Ile Leu Val Asp
1 5 10 15
Val Met Asp Leu Pro Gln Phe Thr Asp Cys Trp Thr Asn Phe Val Asn
20 25 30
Pro Lys Arg Pro Phe Trp Pro Trp Lys Gly Leu Glu
35 40

<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 22
aagtcaaaga aagaaagaca a 21

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 23
aagtcaaaga aagaaagaca a 21

<210> 24
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 24
ttcaggaagg agcccaggtg gctgccatgg acctatacg 39

<210> 25
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 25
ttcaggaagg agcccaggtg gctgccatgg acctatacg 39

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 26
tggtggacgt catggacctc ccac

24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 27
tggtggacgt catggacctc ccac

24

<210> 28
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 28
aatggccaag cgccactcaa aggctgcctg ctaagcgag

39

<210> 29
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 29
aatggccaag cgccactcaa aggctgcctg ctaagcgag

39

<210> 30
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 30
aaaaaactgc ttacaaattt tagataccag gattctaagc ttcaggagat tctgag 56

<210> 31
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 31
aaaagactgc ttacaaattt tagataccag gattctaagc ttcaggagat tctgag 56

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 32
acaaaaggtc tcccagagac gaggttctgc gtggagggca ggcgag 46

<210> 33
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 33
acaaaaggtc tcccagagac gaggttctgg gtggagggca ggtgag 46

<210> 34
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 34
atgggaccat tctgtctggg atgcagccat cgcaaagtct attcaccgat cag 53

<210> 35
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 35
atgggaccat tctgtctggg atgcagccat cgcaaagtct attcaccgat cag 53

<210> 36
<211> 4
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 36
ugau 4

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 37
ttacctgggt ctatggcagt 20

<210> 38
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 38
tgaaggctca gaatcccc 19

<210> 39
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 39
Met Arg Lys Lys Arg Arg Gln Arg Arg Arg Val Asp Ser Leu Leu Met
1 5 10 15

Asn	Arg	Arg	Lys	Phe	Leu	Tyr	Gln	Phe	Lys	Asn	Val	Arg	Trp	Ala	Lys
			20					25					30		
Gly	Arg	Arg	Glu	Thr	Tyr	Leu	Cys	Tyr	Val	Val	Lys	Arg	Arg	Asp	Ser
		35					40					45			
Ala	Thr	Ser	Phe	Ser	Leu	Asp	Phe	Gly	Tyr	Leu	Arg	Asn	Lys	Asn	Gly
	50					55					60				
Cys	His	Val	Glu	Leu	Leu	Phe	Leu	Arg	Tyr	Ile	Ser	Asp	Trp	Asp	Leu
65					70					75					80
Asp	Pro	Gly	Arg	Cys	Tyr	Arg	Val	Thr	Trp	Phe	Thr	Ser	Trp	Ser	Pro
				85					90					95	
Cys	Tyr	Asp	Cys	Ala	Arg	His	Val	Ala	Asp	Phe	Leu	Arg	Gly	Asn	Pro
			100					105					110		
Asn	Leu	Ser	Leu	Arg	Ile	Phe	Thr	Ala	Arg	Leu	Tyr	Phe	Cys	Glu	Asp
		115					120					125			
Arg	Lys	Ala	Glu	Pro	Glu	Gly	Leu	Arg	Arg	Leu	His	Arg	Ala	Gly	Val
	130					135					140				
Gln	Ile	Ala	Ile	Met	Thr	Phe	Lys	Asp	Tyr	Phe	Tyr	Cys	Trp	Asn	Thr
145					150					155					160
Phe	Val	Glu	Asn	His	Glu	Arg	Thr	Phe	Lys	Ala	Trp	Glu	Gly	Leu	His
				165					170					175	
Glu	Asn	Ser	Val	Arg	Leu	Ser	Arg	Gln	Leu	Arg	Arg	Ile	Leu	Leu	Pro
			180					185					190		
Leu	Tyr	Glu	Val	Asp	Asp	Leu	Arg	Asp	Ala	Phe	Arg	Thr	Leu	Gly	Leu
		195				200						205			
His	Ala	Ala	Met	Ala	Asp	Thr	Phe	Leu	Glu	His	Met	Cys	Arg	Leu	Asp
	210				215						220				
Ile	Asp	Ser	Glu	Pro	Thr	Ile	Ala	Arg	Asn	Thr	Gly	Ile	Ile	Cys	Thr
225					230					235					240
Ile	Gly	Pro	Ala	Ser	Arg	Ser	Val	Asp	Lys	Leu	Lys	Glu	Met	Ile	Lys
				245					250					255	
Ser	Gly	Met	Asn	Val	Ala	Arg	Leu	Asn	Phe	Ser	His	Gly	Thr	His	Glu
			260					265					270		
Tyr	His	Glu	Gly	Thr	Ile	Lys	Asn	Val	Arg	Glu	Ala	Thr	Glu	Ser	Phe
		275				280						285			
Ala	Ser	Asp	Pro	Ile	Thr	Tyr	Arg	Pro	Val	Ala	Ile	Ala	Leu	Asp	Thr
	290					295					300				
Lys	Gly	Pro	Glu	Ile	Arg	Thr	Gly	Leu	Ile	Lys	Gly	Ser	Gly	Thr	Ala
305					310					315					320
Glu	Val	Glu	Leu	Lys	Lys	Gly	Ala	Ala	Leu	Lys	Val	Thr	Leu	Asp	Asn
				325					330					335	
Ala	Phe	Met	Glu	Asn	Cys	Asp	Glu	Asn	Val	Leu	Trp	Val	Asp	Tyr	Lys
			340					345					350		
Asn	Leu	Ile	Lys	Val	Ile	Asp	Val	Gly	Ser	Lys	Ile	Tyr	Val	Asp	Asp
		355				360						365			
Gly	Leu	Ile	Ser	Leu	Leu	Val	Lys	Glu	Lys	Gly	Lys	Asp	Phe	Val	Met
	370					375					380				
Thr	Glu	Val	Glu	Asn	Gly	Gly	Met	Leu	Gly	Ser	Lys	Lys	Gly	Val	Asn
385					390					395					400
Leu	Pro	Gly	Ala	Ala	Val	Asp	Leu	Pro	Ala	Val	Ser	Glu	Lys	Asp	Ile
				405					410					415	
Gln	Asp	Leu	Lys	Phe	Gly	Val	Glu	Gln	Asn	Val	Asp	Met	Val	Phe	Ala
			420					425					430		
Ser	Phe	Ile	Arg	Lys	Ala	Ala	Asp	Val	His	Ala	Val	Arg	Lys	Val	Leu
		435					440					445			
Gly	Glu	Lys	Gly	Lys	His	Ile	Lys	Ile	Ile	Ser	Lys	Ile	Glu	Asn	His
	450					455					460				

Glu Gly Val Arg Arg Phe Asp Glu Ile Met Glu Ala Ser Asp Gly Ile
 465 470 475 480
 Met Val Ala Arg Gly Asp Leu Gly Ile Glu Ile Pro Ala Glu Lys Val
 485 490 495
 Phe Leu Ala Gln Lys Met Met Ile Gly Arg Cys Asn Arg Ala Gly Lys
 500 505 510
 Pro Ile Ile Cys Ala Thr Gln Met Leu Glu Ser Met Ile Lys Lys Pro
 515 520 525
 Arg Pro Thr Arg Ala Glu Gly Ser Asp Val Ala Asn Ala Val Leu Asp
 530 535 540
 Gly Ala Asp Cys Ile Met Leu Ser Gly Glu Thr Ala Lys Gly Asp Tyr
 545 550 555 560
 Pro Leu Glu Ala Val Arg Met Gln His Ala Ile Ala Arg Glu Ala Glu
 565 570 575
 Ala Ala Met Phe His Arg Gln Gln Phe Glu Glu Ile Leu Arg His Ser
 580 585 590
 Val His His Arg Glu Pro Ala Asp Ala Met Ala Ala Gly Ala Val Glu
 595 600 605
 Ala Ser Phe Lys Cys Leu Ala Ala Leu Ile Val Met Thr Glu Ser
 610 615 620
 Gly Arg Ser Ala His Leu Val Ser Arg Tyr Arg Pro Arg Ala Pro Ile
 625 630 635 640
 Ile Ala Val Thr Arg Asn Asp Gln Thr Ala Arg Gln Ala His Leu Tyr
 645 650 655
 Arg Gly Val Phe Pro Val Leu Cys Lys Gln Pro Ala His Asp Ala Trp
 660 665 670
 Ala Glu Asp Val Asp Leu Arg Val Asn Leu Gly Met Asn Val Gly Lys
 675 680 685
 Ala Arg Gly Phe Phe Lys Thr Gly Asp Leu Val Ile Val Leu Thr Gly
 690 695 700
 Trp Arg Pro Gly Ser Gly Tyr Thr Asn Thr Met Arg Val Val Pro Val
 705 710 715 720
 Pro Leu Glu Tyr Pro Tyr Asp Val Pro Asp Tyr Ala His His His His
 725 730 735
 His His

<210> 40

<211> 2217

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 40

atgagaaaaa	aaagaagaca	aagaagaaga	gtggacagcc	tcttgatgaa	ccggaggaag	60
tttctttacc	aattcaaaaa	tgtccgctgg	gctaagggtc	ggcgtgagac	ctacctgtgc	120
tacgtagtga	agaggcgtga	cagtgtctaca	tccttttcac	tggactttgg	ttatcttcgc	180
aataagaacg	gctgccacgt	ggaattgctc	ttcctccgct	acatctcgga	ctgggaccta	240
gaccttgccc	gctgtaccg	cgtcacctgg	ttcacctcct	ggagcccctg	ctacgactgt	300
gcccgcacatg	tggccgactt	tctgcgaggg	aaccccaacc	tcagtctgag	gatcttcacc	360
gcgcgcctct	acttctgtga	ggaccgcaag	gctgagcccg	aggggctgcg	gcggctgcac	420
cgcgcggggg	tgcaaatagc	catcatgacc	ttcaaagatt	atcttttactg	ctggaatact	480
tttgtagaaa	accatgaaa	aactttcaaa	gcctgggaag	ggctgcatga	aaattcagtt	540

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cgtctctcca gacagcttcg acgaatcctt ttgcccctgt atgaggttga tgacttacga      600
gacgcatttc gtactttggg acttcacgct gccatggcag acacctttct ggagcacatg      660
tgccgcctgg acatcgactc cgagccaacc attgccagaa acaccggcat catctgcacc      720
atcggccccag cctcccgcctc tgtggacaag ctgaaggaaa tgattaaatc tggaatgaat      780
gttgcgccgcc tcaacttctc gcacggcacc cacgagtatc atgagggcac aattaagaac      840
gtgcgagagg ccacagagag ctttgcctct gacccgatca cctacagacc tgtggctatt      900
gcactggaca ccaaggggacc tgaatccga actggactca tcaaggaag tggcacagca      960
gaggtggagc tcaagaaggg cgagctctc aaagtgacgc tggacaatgc cttcatggag     1020
aactgcgatg agaatgtgct gtgggtggac tacaagaacc tcatcaaagt tatagatgtg     1080
ggcagcaaaa tctatgtgga tgacggtctc atttccttgc tggttaagga gaaaggcaag     1140
gactttgtca tgactgaggt tgagaacggt ggcattgctg gtagtaagaa gggagtgaac     1200
ctcccagggt ctgcggtcga cctgcctgca gtctcagaga aggacattca ggacctgaaa     1260
tttggcgtgg agcagaatgt ggacatggtg ttgccttctc tcatccgcaa agctgctgat     1320
gtccatgctg tcaggaaggt gctaggggaa aagggaaagc acatcaagat tatcagcaag     1380
attgagaatc acgaggtgtg gcgcaggttt gatgagatca tggaggccag cgatggcatt     1440
atggtggccc gtggtgacct gggattagag atccctgctg aaaaagtctt cctcgcacag     1500
aagatgatga ttgggcgctg caacagggtt ggcaaaccce tcatttgtgc cactcagatg     1560
ttggaaagca tgatcaagaa acctcgcccg acccgcgctg agggcagtg tgttgccaat     1620
gcagttctgg atggagcaga ctgcatcatg ctgtctgggg agaccgcaa gggagactac     1680
ccactggagg ctgtgcgatg gcagcacgct attgctcgct aggctgaggg cgcaatgttc     1740
catcgtcagc agtttgaaga aatcttacgc cacagtgtac accacagggg gcctgctgat     1800
gccatggcag caggcgcggt ggaggcctcc tttaagtgtc tagcagcagc tctgatagtt     1860
atgaccgagt ctggcaggtc tgcacacctg gtgtcccggg accgcccgcg ggctcccatc     1920
atcgccgtca cccgcaatga ccaaacagca cgccaggcac acctgtaccg cggcgtcttc     1980
cccgtgctgt gcaagcagcc ggcccacgat gcctgggcag aggatgtgga tctccgtgtg     2040
aacctgggca tgaatgtcgg caaagcccgt ggattcttca agaccgggga cctggtgatc     2100
gtgctgacgg gctggcgccc cggtctccggc tacaccaaca ccatgcgggt ggtgcccgtg     2160
ccactcgagt acccctacga cgtgcccgac tacgcccacc accaccacca ccactga      2217

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<210> 41

<211> 530

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 41

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Met Ser Lys His His Asp Ala Gly Thr Ala Phe Ile Gln Thr Gln Gln
 1           5           10          15
Leu His Ala Ala Met Ala Asp Thr Phe Leu Glu His Met Cys Arg Leu
          20          25          30
Asp Ile Asp Ser Glu Pro Thr Ile Ala Arg Asn Thr Gly Ile Ile Cys
          35          40          45
Thr Ile Gly Pro Ala Ser Arg Ser Val Asp Lys Leu Lys Glu Met Ile
          50          55          60
Lys Ser Gly Met Asn Val Ala Arg Leu Asn Phe Ser His Gly Thr His
65          70          75          80
Glu Tyr His Glu Gly Thr Ile Lys Asn Val Arg Glu Ala Thr Glu Ser
          85          90          95
Phe Ala Ser Asp Pro Ile Thr Tyr Arg Pro Val Ala Ile Ala Leu Asp
          100         105         110
Thr Lys Gly Pro Glu Ile Arg Thr Gly Leu Ile Lys Gly Ser Gly Thr
          115         120         125
Ala Glu Val Glu Leu Lys Lys Gly Ala Ala Leu Lys Val Thr Leu Asp

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130	135	140
Asn Ala Phe Met Glu	Asn Cys Asp Glu	Asn Val Leu Trp Val Asp Tyr
145	150	155
Lys Asn Leu Ile Lys	Val Ile Asp Val Gly	Ser Lys Ile Tyr Val Asp
165	170	175
Asp Gly Leu Ile Ser	Leu Leu Val Lys	Glu Lys Gly Lys Asp Phe Val
180	185	190
Met Thr Glu Val Glu	Asn Gly Gly Met	Leu Gly Ser Lys Lys Gly Val
195	200	205
Asn Leu Pro Gly Ala	Ala Val Asp Leu	Pro Ala Val Ser Glu Lys Asp
210	215	220
Ile Gln Asp Leu Lys	Phe Gly Val Glu	Gln Asn Val Asp Met Val Phe
225	230	235
Ala Ser Phe Ile Arg	Lys Ala Ala Asp	Val His Ala Val Arg Lys Val
245	250	255
Leu Gly Glu Lys Gly	Lys His Ile Lys	Ile Ile Ser Lys Ile Glu Asn
260	265	270
His Glu Gly Val Arg	Arg Phe Asp Glu	Ile Met Glu Ala Ser Asp Gly
275	280	285
Ile Met Val Ala Arg	Gly Asp Leu Gly	Ile Glu Ile Pro Ala Glu Lys
290	295	300
Val Phe Leu Ala Gln	Lys Met Met Ile	Gly Arg Cys Asn Arg Ala Gly
305	310	315
Lys Pro Ile Ile Cys	Ala Thr Gln Met	Leu Glu Ser Met Ile Lys Lys
325	330	335
Pro Arg Pro Thr Arg	Ala Glu Gly Ser	Asp Val Ala Asn Ala Val Leu
340	345	350
Asp Gly Ala Asp Cys	Ile Met Leu Ser	Gly Glu Thr Ala Lys Gly Asp
355	360	365
Tyr Pro Leu Glu Ala	Val Arg Met Gln	His Ala Ile Ala Arg Glu Ala
370	375	380
Glu Ala Ala Met Phe	His Arg Gln Gln	Phe Glu Glu Ile Leu Arg His
385	390	395
Ser Val His His Arg	Glu Pro Ala Asp	Ala Met Ala Ala Gly Ala Val
405	410	415
Glu Ala Ser Phe Lys	Cys Leu Ala Ala	Ala Leu Ile Val Met Thr Glu
420	425	430
Ser Gly Arg Ser Ala	His Leu Val Ser	Arg Tyr Arg Pro Arg Ala Pro
435	440	445
Ile Ile Ala Val Thr	Arg Asn Asp Gln	Thr Ala Arg Gln Ala His Leu
450	455	460
Tyr Arg Gly Val Phe	Pro Val Leu Cys	Lys Gln Pro Ala His Asp Ala
465	470	475
Trp Ala Glu Asp Val	Asp Leu Arg Val	Asn Leu Gly Met Asn Val Gly
485	490	495
Lys Ala Arg Gly Phe	Phe Lys Thr Gly	Asp Leu Val Ile Val Leu Thr
500	505	510
Gly Trp Arg Pro Gly	Ser Gly Tyr Thr	Asn Thr Met Arg Val Val Pro
515	520	525
Val Pro		
530		

<210> 42

<211> 1593

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 42

atgtcgaagc	accacgatgc	agggaccgct	ttcatccaga	cccagcagct	gcacgctgcc	60
atggcagaca	cctttctgga	gcacatgtgc	cgcttgga	tcgactccga	gccaaccatt	120
gccagaaaca	ccggcatcat	ctgcaccatc	ggcccagcct	cccgtctgtg	ggacaagctg	180
aaggaaatga	ttaaattctgg	aatgaatggt	gcccgcctca	acttctcgca	cggcaccac	240
gagtatcatg	agggcacaat	taagaacgtg	cgagaggcca	cagagagctt	tgcctctgac	300
ccgatcacct	acagacctgt	ggctattgca	ctggacacca	agggacctga	aatccgaact	360
ggactcatca	agggaggtgg	cacagcagag	gtggagctca	agaagggcgc	agctctcaaa	420
gtgacgctgg	acaatgcctt	catggagaac	tgcgatgaga	atgtgctgtg	ggtggactac	480
aagaacctca	tcaaagttat	agatgtgggc	agcaaaatct	atgtggatga	cgtctcatt	540
tccttgctgg	ttaaggagaa	aggcaaggac	tttgtcatga	ctgaggttga	gaacgggtggc	600
atgcttggtg	gtaagaaggg	agtgaacctc	ccaggtgctg	cggtcgacct	gcctgcagtc	660
tcagagaagg	acattcagga	cctgaaattt	ggcgtggagc	agaatgtgga	catggtgttc	720
gcttccttca	tccgcaaagc	tgctgatgtc	catgctgtca	ggaaggtgct	aggggaaaag	780
ggaaagcaca	tcaagattat	cagcaagatt	gagaatcacg	aggtgtgctg	caggtttgat	840
gagatcatgg	aggccagcga	tggcattatg	gtggcccgtg	gtgacctggg	tattgagatc	900
cctgctgaaa	aagtcttcct	cgcacagaag	atgatgattg	ggcgtgcaa	cagggctggc	960
aaacccatca	tttgtgccac	tcagatgttg	gaaagcatga	tcaagaaacc	tcgcccagacc	1020
cgcgtgagg	gcagtgatgt	tgccaatgca	gttctggatg	gagcagactg	catcatgctg	1080
tctggggaga	ccgccaaggg	agactaccca	ctggaggctg	tgcgcatgca	gcacgctatt	1140
gctcgtgagg	ctgaggccgc	aatgttccat	cgtcagcagt	ttgaagaaat	cttacgccac	1200
agtgtacacc	acaggagacc	tgctgatgcc	atggcagcag	gcgcggtgga	ggcctccttt	1260
aagtgttag	cagcagctct	gatagttatg	accgagtctg	gcaggtctgc	acacctggtg	1320
tcccgttacc	gcccgcgggc	tcccatcatc	gccgtcacc	gcaatgacca	aacagcacgc	1380
caggcacacc	tgtaccgcgg	cgtcttcccc	gtgctgtgca	agcagccggc	ccacgatgcc	1440
tgggcagagg	atgtggatct	ccgtgtgaac	ctgggcatga	atgtcggcaa	agcccgtgga	1500
ttcttcaaga	ccggggacct	ggtgatcgtg	ctgacgggct	ggcgcccccg	ctccggctac	1560
accaacacca	tcgggggtgt	gcccgtgcca	tga			1593

<210> 43

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 43

Arg Lys Lys Arg Arg Gln Arg Arg Arg

1

5

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 44
agaaaaaaaaa gaagacaaag aagaaga

27

<210> 45
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 45
Met Thr Ser Glu Lys Gly Pro Ser Thr Gly Asp Pro Thr Leu Arg Arg
1 5 10 15
Arg Ile Glu Pro Trp Glu Phe Asp Val Phe Tyr Asp Pro Arg Glu Leu
20 25 30
Arg Lys Glu Ala Cys Leu Leu Tyr Glu Ile Lys Trp Gly Met Ser Arg
35 40 45
Lys Ile Trp Arg Ser Ser Gly Lys Asn Thr Thr Asn His Val Glu Val
50 55 60
Asn Phe Ile Lys Lys Phe Thr Ser Glu Arg Asp Phe His Pro Ser Ile
65 70 75 80
Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Trp Glu Cys
85 90 95
Ser Gln Ala Ile Arg Glu Phe Leu Ser Arg His Pro Gly Val Thr Leu
100 105 110
Val Ile Leu Tyr Val Ala Arg Leu Phe Trp His Met Asp Gln Gln Asn
115 120 125
Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln Ile
130 135 140
Met Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe Val Asn Tyr
145 150 155 160
Pro Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro Pro Leu Trp Met
165 170 175
Met Leu Tyr Ala Leu Glu Leu His Cys Ile Ile Leu Ser Leu Pro Pro
180 185 190
Cys Leu Lys Ile Ser Arg Arg Trp Gln Asn His Leu Thr Phe Phe Arg
195 200 205
Leu His Leu Gln Asn Cys His Tyr Gln Thr Ile Pro Pro His Ile Leu
210 215 220
Leu Ala Thr Gly Leu Ile His Pro Ser Val Ala Trp Arg
225 230 235

<210> 46
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 46
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 47
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 47
 taccctacg acgtgcccga ctacgcc

27

<210> 48
 <211> 429
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 48
 Met Gly Pro Phe Cys Leu Gly Cys Ser His Arg Lys Cys Tyr Ser Pro
 1 5 10 15
 Ile Arg Asn Leu Ile Ser Gln Glu Thr Phe Lys Phe His Phe Lys Asn
 20 25 30
 Leu Arg Tyr Ala Ile Asp Arg Lys Asp Thr Phe Leu Cys Tyr Glu Val
 35 40 45
 Thr Arg Lys Asp Cys Asp Ser Pro Val Ser Leu His His Gly Val Phe
 50 55 60
 Lys Asn Lys Asp Asn Ile His Ala Glu Ile Cys Phe Leu Tyr Trp Phe
 65 70 75 80
 His Asp Lys Val Leu Lys Val Leu Ser Pro Arg Glu Glu Phe Lys Ile
 85 90 95
 Thr Trp Tyr Met Ser Trp Ser Pro Cys Phe Glu Cys Ala Glu Gln Val
 100 105 110
 Leu Arg Phe Leu Ala Thr His His Asn Leu Ser Leu Asp Ile Phe Ser
 115 120 125
 Ser Arg Leu Tyr Asn Ile Arg Asp Pro Glu Asn Gln Gln Asn Leu Cys
 130 135 140
 Arg Leu Val Gln Glu Gly Ala Gln Val Ala Ala Met Asp Leu Tyr Glu
 145 150 155 160
 Phe Lys Lys Cys Trp Lys Lys Phe Val Asp Asn Gly Gly Arg Arg Phe
 165 170 175
 Arg Pro Trp Lys Lys Leu Leu Thr Asn Phe Arg Tyr Gln Asp Ser Lys
 180 185 190
 Leu Gln Glu Ile Leu Arg Pro Cys Tyr Ile Pro Val Pro Ser Ser Ser
 195 200 205
 Ser Ser Thr Leu Ser Asn Ile Cys Leu Thr Lys Gly Leu Pro Glu Thr
 210 215 220
 Arg Phe Cys Val Glu Gly Arg Arg Val His Leu Ser Glu Glu Glu
 225 230 235 240
 Phe Tyr Ser Gln Phe Tyr Asn Gln Arg Val Lys His Leu Cys Tyr Tyr
 245 250 255

His Gly Met Lys Pro Tyr Leu Cys Tyr Gln Leu Glu Gln Phe Asn Gly
 260 265 270
 Gln Ala Pro Leu Lys Gly Cys Leu Leu Ser Glu Lys Gly Lys Gln His
 275 280 285
 Ala Glu Ile Leu Phe Leu Asp Lys Ile Arg Ser Met Glu Leu Ser Gln
 290 295 300
 Val Ile Ile Thr Cys Tyr Leu Thr Trp Ser Pro Cys Pro Asn Cys Ala
 305 310 315 320
 Trp Gln Leu Ala Ala Phe Lys Arg Asp Arg Pro Asp Leu Ile Leu His
 325 330 335
 Ile Tyr Thr Ser Arg Leu Tyr Phe His Trp Lys Arg Pro Phe Gln Lys
 340 345 350
 Gly Leu Cys Ser Leu Trp Gln Ser Gly Ile Leu Val Asp Val Met Asp
 355 360 365
 Leu Pro Gln Phe Thr Asp Cys Trp Thr Asn Phe Val Asn Pro Lys Arg
 370 375 380
 Pro Phe Trp Pro Trp Lys Gly Leu Glu Ile Ile Ser Arg Arg Thr Gln
 385 390 395 400
 Arg Arg Leu His Arg Ile Lys Glu Ser Trp Gly Leu Gln Asp Leu Val
 405 410 415
 Asn Asp Phe Gly Asn Leu Gln Leu Gly Pro Pro Met Ser
 420 425

<210> 49

<211> 1948

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 49

acttggccccg	ggaggtcagt	ttcactttctg	gggggtcttcc	atagcctgct	cacagaaaat	60
gcaacccccag	cgcatggggc	ccagagctgg	gatggggacca	ttctgtcttg	gatgcagcca	120
tcgcaaatgc	tattcaccga	tcagaaacct	gatatctcaa	gaaacattca	aattccactt	180
taagaacct	cgctatgcca	tagaccggaa	agataccttc	ttgtgctatg	aagtgcactg	240
aaaggactgc	gattcacccg	tctcccttca	ccatgggggtc	tttaagaaca	aggacaacat	300
ccacgctgaa	atctgctttt	tatactgggt	ccatgacaaa	gtactgaaag	tgctgtctcc	360
gagagaagag	ttcaagatca	cctgggtatat	gtcctggagc	ccctgtttcg	aatgtgcaga	420
gcaggtacta	aggttcctgg	ctacacacca	caacctgagc	ctggacatct	tcagctccccg	480
cctctacaac	atacgggacc	cagaaaacca	gcagaatctt	tgcaggctgg	ttcaggaagg	540
agcccaggtg	gctgccatgg	acctatacga	atttaaaaag	tgttggaaga	agtttggtgga	600
caatggcggc	aggcgattca	ggccttgga	aaaactgctt	acaaatttta	gataccagga	660
ttctaagctt	caggagattc	tgagaccttg	ctacatcccg	gtcccttcca	gctcttcac	720
cactctgtca	aatatctgtc	taacaaaagg	tctcccagag	acgaggttct	gcgtggaggg	780
caggcgagtg	cacctgttaa	gtgaagagga	attttactcg	cagttttaca	accaacgagt	840
caagcatctc	tgctactacc	acggcatgaa	gccctatcta	tgctaccagc	tggagcagtt	900
caatggccaa	gcgccactca	aaggctgcct	gctaagcgag	aaaggcaaac	agcatgcaga	960
aatcctcttc	cttgataaga	ttcgggtccat	ggagctgagc	caagtgataa	tcacctgcta	1020
cctcacctgg	agcccctgcc	caaactgtgc	ctggcaactg	gcggcattca	aaagggatcg	1080
tccagatcta	attctgcata	tctacacctc	ccgcctgtat	ttccactgga	agaggccctt	1140
ccagaagggg	ctgtgtttct	tgtggcaatc	agggatcctg	gtggacgtca	tggacctccc	1200
acagtttact	gactgctgga	caaactttgt	gaaccggaaa	aggccgtttt	ggccatggaa	1260
aggattggag	ataatcagca	ggcgcacaca	aaggcggctc	cacaggatca	aggagtcctg	1320
gggtctgcaa	gatttgggtga	atgacttttg	aaacctacag	cttggacccc	cgatgtcttg	1380

agaggcaaga	agagattcaa	gaaggtcttt	tggtgacccc	cccacccaac	cccaagtcta	1440
ggagaccttt	tgttctcccg	tttgtttccc	cttttgtttt	atcttttggt	gttttgcttt	1500
gttttgaaga	cagagtctca	ctgggtagct	tgctactctg	gaactcacta	ctagactaag	1560
ctggccttaa	actctaaaaat	ccacctgcca	atgccttctg	agagccaggc	ttaaggtgtg	1620
cgctgcccac	tcccagcctt	aaccactgt	ggcttttctt	tcctctttct	tttattatct	1680
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